



Supplementary Figure 2. The majority of reads mapping to *B. hordei* or *H. vulgare* originate from transposable elements or coding genes. We assigned reads aligning to the genomes of (A) *B. hordei* or (B) *H. vulgare* to the features mRNA (coding genes; light blue/green), miRNA loci identified in this study (blue/green), and transposable elements (dark blue/green). We plotted the read length (x-axis) against the respective number of reads (y-axis). The six sample types were epiphytic fungal mycelium (MYC), infected epidermis without mycelium (EPI), fungal haustoria (HAU), microsomes of the epidermis without haustoria (P40), apoplastic extracellular vesicles (EV+), and apoplastic extracellular vesicles of non-infected control plants (EV-).